Stabilizing and Understanding a Miniprotein by Rational Redesign

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Supporting Information Placeholder

ABSTRACT: Miniproteins reduce the complexity of the protein-folding problem allowing systematic studies of contributions to protein folding and stabilization. Here, we describe the rational redesign of a miniprotein, PPα, comprising a polyproline-II helix, loop and α helix. The redesign provides a *de novo* framework to interrogate non-covalent interactions. Optimized PPα has significantly improved thermal stability with a midpoint unfolding temperature (T_M) of 51°C. Its NMR structure indicates a higher density of stabilizing non-covalent interactions than the parent peptide, specifically increased CH–π interactions. In part, we attribute this to improved long-range electrostatic interactions between the two helical elements. We probe further sequence-to-stability relationships in the miniprotein through a series of rational mutations.

The primary sequence of a protein determines its three-dimensional structure and function. Understanding sequence-to-structure relationships is known as the protein-folding problem.[1] Studying miniproteins reduces the complexity of the problem, allowing contributions to protein folding and stability to be dissected more easily.[2, 3] Prominent examples of miniproteins include: the Trp-cage,[4] βαβ motifs,[5] villin headpiece,[6] pancreatic peptides[7-10] and the Trp-Plexus.[11] The formation of many weak and cooperative non-covalent interactions is central to protein stability, allowing the loss of conformational entropy upon folding to be overcome. This is particularly important for miniproteins with fewer interactions possible.[12]

α Helices are common building blocks in proteins. They are often stabilized by tertiary and quaternary interactions, as exemplified in α-helical coiled coils, a ubiquitous folding motif comprising two or more α helices supercoiled around each other.[13] Most coiled-coil sequences have a seven-residue heptad repeat, ***abcdefg***, with hydrophobic residues at ***a*** and ***d***, and polar residues at the remaining sites. This pattern leads to the association of helices *via* "knobs-into-holes" packing interactions, where side chains of one helix dock into diamond-shaped holes of another.[14, 15] α Helices can also be stabilized by the interdigitation of proline (Pro, P) from polyproline-II helices between aromatic residues on α helices, which are analogous to knobs-into-holes packing.[2, 7, 16]

Elsewhere, we describe the fragment-based design of a 34-residue miniprotein, PPα.[17] This comprises a polyproline-II helix, loop and α helix adapted from natural proteins (Figure 1A,B).[7, 16] PPα is monomeric in aqueous solution and unfolds reversibly with a T_M of 39 ˚C. A solution NMR structure shows the stabilizing effect of Pro and tyrosine (Tyr, Y) interdigitation and associated CH–π interactions. In the latter, protons of C–H bonds interact with aromatic rings.[17-20] Here, we explore the optimization of PPα by rational redesign, revealing sequence-to-stability relationships for the miniprotein fold and delivering a *de novo* framework of significantly enhanced thermal stability.

In the design of α-helical coiled coils, charged residues often flank the hydrophobic core and form inter-helical Coulombic interactions.[2] We reasoned that PPα might be stabilized by introducing similar interactions between the ***2*** and ***3*** positions of the polyproline-II helix and the ***e*** and ***g*** positions of the α helix (Figure 1A,C).

There are two extreme possibilities for pairing charged residues in PPα: a lysine (Lys, K)-based polyproline-II helix and a glutamic acid (Glu, E)-based α helix or *vice versa* (PPα-KE and PPα-EK, respectively, Table 1). We optimized helix propensity for the solvent-exposed face of the α helix by placing alanine (Ala, A) at ***b*** and ***c*** and Lys at ***f*** in both designs.

Otherwise, the helix-helix interface was maintained, with Pro at ***1***, leucine (Leu, L) at ***a*** and Tyr at ***d***., along with the PPα loop. We adopted the coiled-coil heptad nomenclature for the α-helical sequence as it has a 7-residue repeat.

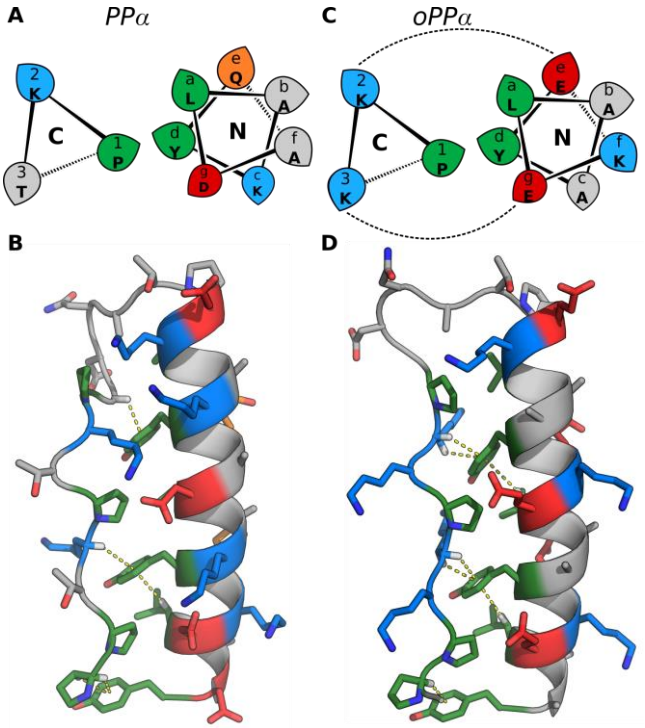

Figure 1. Helical wheel representations for the two helices in PPα (A) and PPα-KE (oPPα) (C). Leaf tips indicate the direction of the Cα-Cβ bond vectors. Lowercase letters on the α helix and numbers on the polyproline-II helix denote the helical register. C and N refer to the helix termini nearest the viewer. Dashed black lines: long-range interhelical electrostatic interactions. Representative models from the NMR ensembles of PPα (B, PDB entry 5LO2, model 14) and PPα-KE (D, PDB entry 6GWX, model 8). Dashed yellow lines: CH–π interactions. Key: Lys (blue), Glu/Asp (red), and Tyr/Pro/Leu (green), Gln (orange).

PPα-KE and PPα-EK were synthesized by solid-phase peptide synthesis, purified by reverse-phase HPLC, and confirmed by MALDI-TOF mass spectrometry (Figure S1A,B). Circular dichroism (CD) spectroscopy revealed both peptides were 50% α helical at 5 °C like PPα (Figure 2A). Sedimentation equilibrium analytical ultracentrifugation (AUC) showed that both peptides were monomeric (Figure S3A,B). PPα-KE had cooperative and reversible thermal unfolding transitions when followed by far- and near-UV CD (Figure S2U,V), and the T_M (51 °C) was substantially increased over PPα (39 °C). However, PPα-EK was less stable than PPα-KE by 10 °C (Figure 2B). We posit that the reduced stability of PPα-EK stems from the large charge on the α helix—+6 compared to -2 for PPα-KE—and different propensities of Glu and Lys for α and polyproline-II helices (Table S1,2).[21,22]

High-resolution NMR spectroscopy was used to determine the solution-phase structure of PPα-KE (Figure 1D), with 95.8% of the ^{1}H NMR resonances assigned. The core of the structure was well defined, while several of the solvent-exposed residues were more dynamic. The root-mean-square deviations (RMSDs) across the 20 structures of the ensemble were 0.52 ± 0.13 Å (backbone) and 1.05 ± 0.15 Å (all atom), comparable to those for the structure of PPα (Table S3).[17] A representative structure matched PPα with backbone and all-atom RMSDs of 0.5 Å and 0.9 Å, respectively.

The average distances between N_ζ of Lys and C_δ of Glu introduced in PPα-KE were 8.7 ± 1.8 Å and 11.5 ± 2.4 Å for ***2:e*** and ***3:g***, respectively. These fall outside of any accepted definition of salt-bridge interactions,[23] suggesting longer-range electrostatic interactions may stabilize the folded state of PPα-KE. To test this, the thermal stability of PPα-KE was measured at different salt concentrations in phosphate buffer (Figure S2C,D). With increased concentrations of NaCl from 0 to 700 mM the T_M fell from 61 to 57 °C (Figure S2W), indicative of an electrostatic component to thermostability.

As PPα is stabilized by CH–π interactions,[17] we searched for these in PPα-KE. This revealed 87 CH–π interactions across the ensemble (4.35 per structure), an increase over PPα (68 CH–π interactions; 3.4 per structure) (Figure 1B,D, Table S5 and Figure S8). A shift in CH donors between the two miniproteins was also observed. In PPα-KE fewer CH donors emanated from Pro residues (PPα-KE, 5; PPα, 22), but more arose from Leu (PPα-KE, 25; PPα, 4) and Lys residues (PPα-KE, 57; PPα, 15). On closer inspection, the side chains of Lys4 and Lys7 of PPα-KE lie across the faces of Tyr27 and Tyr20, respectively, leading to CH–π interactions between the C_α and C_β protons of the former and the aromatic rings of the latter. To test for CH–π interactions experimentally, we replaced all of the electron-rich Tyr residues in PPα-KE by more-electron-poor phenylalanine (Phe, F) giving PPα-KE-Phe (Table 1). As with PPα,[17] this reduced the T_M by approximately 20 °C (Figure S2E,F). This indicates that CH–π interactions are at play in PPα-KE in addition to van der Waals' forces.

Overall, we posit that the improved stability of PPα-KE arises from increased long-range electrostatic interactions between the polyproline-II and α helix,[24-27] which lead to an increased density of shorter-range CH–π interactions.

Tyr residues at the ***d*** sites of the 7-residue repeats of PPα and related natural folds are critical for folding and stability.[7, 16, 17] These residues form two vertices of 4-residue 'holes' defined by side chains at successive ***d***, ***a***, ***g***, and ***d*** sites, which accommodate Pro 'knobs' from the polyproline-II helix. In PPα and PPα-KE, the ***g*** site is fixed as aspartic acid (Asp, D) or Glu, respectively. The ***a*** sites are all Leu, which is the preferred residue in natural sequences.[7, 28] To explore possible substitutes for Leu at ***a***, we made mutants with all three ***a*** sites replaced by: β-branched, isoleucine (Ile, I) or valine (Val, V); charged,

Table 1. Designed peptides and summary of biophysical data.

Peptide	Sequence and helical register *321321321321321 efgabcd efgabcd efgabcd efgabcd efgabcd*	TM / °C	AUC *
Parent PPα	PPTKPTKP GDNAT PEKLAKY QADLAKY QKDLADY	39	0.9
PPα-KE/oPPα	PPKKPKKP GDNAT PEKLAAY EKELAAY EKELAAY	51	1.0
PPα-EK	PP**EE**P**EE**P GDNAT PEKLAAY **KK**K**K**LAAY **KK**K**K**LAAY	40	0.9
PPα-KE-Phe	PPKKPKKP GDNAT PEKLAA**F** EKELAA**F** EKELAA**F**	33	1.0
PPα-KE-E@a	PPKKPKKP GDNAT PEK**E**AAY EKE**E**AAY EKE**E**AAY	-	-
PPα-KE-A@a	PPKKPKKP GDNAT PEK**A**AAY EKE**A**AAY EKE**A**AAY	-	1.0
PPα-KE-K@a	PPKKPKKP GDNAT PEK**K**AAY EKE**K**AAY EKE**K**AAY	19	1.0
PPα-KE-I@a	PPKKPKKP GDNAT PEK**I**AAY EKE**I**AAY EKE**I**AAY	40	1.0
PPα-KE-V@a	PPKKPKKP GDNAT PEK**V**AAY EKE**V**AAY EKE**V**AAY	34	1.0
PPα-KE-A@g	PPKKPKKP GDNAT PEKLA**E**Y EK**A**LA**E**Y EK**A**LA**E**Y	21	1.0
PPα-KE-L@g	PPKKPKKP GDNAT PEKLA**E**Y EK**L**LA**E**Y EK**L**LA**E**Y	76	1.2
PPα-KE-a↔g	PPKKPKKP GDNAT PEKLAAY **AALEKE**Y **AALEKE**Y	19	1.1
oPPα-2	PPKKP GDNAT PEKLAAY EKELAAY	19	0.9
oPPα-4	PPKKPKKPKKP GDNAT PEKLAAY EKELAAY EKELAAY EKELAAY	66	1.0
oPPα-5	PPKKPKKPKKPKKP GDNAT PEKLAAY EKELAAY EKELAAY EKELAAY EKELAAY	72	1.0
oPPα-5-skip	PPKKPKKPPKKPKKP GDNAT PEKLAAY EKELAAY EKELAAY EKELAAY EKELAAY	68	1.0

Peptides were capped with *N*-terminal acetyl and *C*-terminal amide groups. *Oligomeric state (× monomer mass) as determined by AUC. Mutations to the PPα-KE/oPPα interface are shown in bold.

Glu or Lys; or Ala (Table 1).

AUC confirmed that these PPα-KE-X@***a*** mutants were monomeric in solution (Figure S3). However, CD spectroscopy revealed a range of stabilities. PPα-KE-E@***a*** was not folded, possibly due to the proximal glutamates at ***e*** if the α helix were folded. The stabilities of PPα-KE-A@***a*** and PPα-KE-K@***a*** were compromised compared to PPα-KE (Figure 2C,D). By contrast, both PPα-KE-I@***a*** and PPα-KE-V@***a*** were folded, albeit with reduced thermal stabilities compared with PPα-KE. This suggests that the extra steric bulk of the β carbon may hinder docking of Pro into the hole, although we note that α-helical propensities of both Ile and Val are also lower than that of Leu.[21]

We also probed the ***g*** position of the hole, initially *via* an Ala mutation to determine the contribution of this residue to stability. To maintain the introduced electrostatic interactions between the helices, Glu was shifted to the ***c*** position, although this may introduce favorable $K_i \rightarrow E_{i+4}$ interactions. The resulting PPα-KE-A@g was monomeric, but significantly less stable than PPα-KE (Figure S2I,J). Next, we mutated the ***g*** position to Leu, giving a fully hydrophobic hole. The thermal unfolding transition of PPα-KE-L@***g*** was broad, with a T_M of 76 °C (Figure S2K,L). However, the CD signal was concentration dependent, indicating aggregation (Figure S2M,N). AUC experiments returned a mass of 1.2 × monomer mass, suggesting PPα-KE-L@***g*** forms higher-order species, which could involve the wider hydrophobic interface. Our interests lie in fully monomeric miniproteins, so the ***g*** positions were not probed further.

As a final exploration of hole-residue preferences, we swapped the ***a*** and ***g*** residues (PPα-KE-***a*↔*g***). This tests an alternate helical register, LXXXYXX, as opposed to LXXYXXX in PPα-KE. Residues at ***e*** and ***c***, and ***b*** and ***f*** were swapped to avoid introducing charged interactions in the α helix of PPα-KE-***a*↔*g*** not present

in PPα-KE. PPα-KE-***a*↔*g*** was less folded and less thermally stable (T_M 19 °C) than PPα-KE. Thus, PPα-KE possesses the optimal arrangement of residues in the diamond-shaped hole.

The results of this mutagenesis study reveal that Leu at ***a***, Tyr at ***d*** and Glu at ***g*** provide the optimal 'hole' to accommodate Pro in PPα-like miniproteins. On this basis, we renamed PPα-KE as optimised-PPα, oPPα.

Using oPPα, we investigated the effect of helix length on stability. Variants were synthesised with 1-, 3- and 4-unit polyproline-II-helical repeats and corresponding 2-, 4- and 5- heptad α-helical repeats (Table 1, Figure S15). Like oPPα, which completes this series with two polyproline-II and three

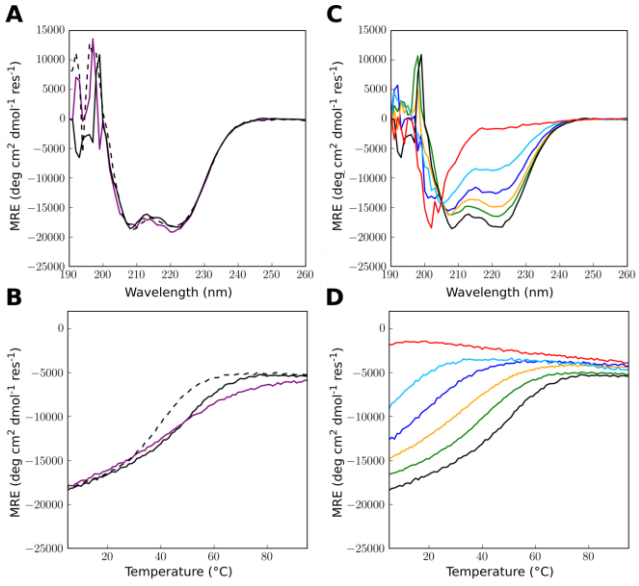

Figure 2. Folding and stability of PPα-KE and mutants. Far-UV CD spectra at 5 °C for: (A) parent PPα (black, dash), PPα-KE (black), and PPα-EK (purple); and (C) PPα-KE-E@a (red), PPα-KE-A@a (sky blue), PPα-KE-K@a (blue), PPα-KE-I@a (green), PPα-KE-V@a (orange), and PPα-KE (black). (B&D) Temperature dependence of the mean residue ellipticity (MRE) at 222 nm, with the key as for panels A&C. Conditions: 100 μM peptide, PBS, pH 7.4.

α-helical repeats, these peptides were monomers (Figure S3M,N,O). However, only oPPα, oPPα-4 and oPPα-5 were appreciably and stably folded (Figure 3), with the T_M increasing from 51 to 66 to 72 °C, respectively. As observed in α-helical coiled coils, folding and stability increases in a non-linear, cooperative manner.[29, 30]

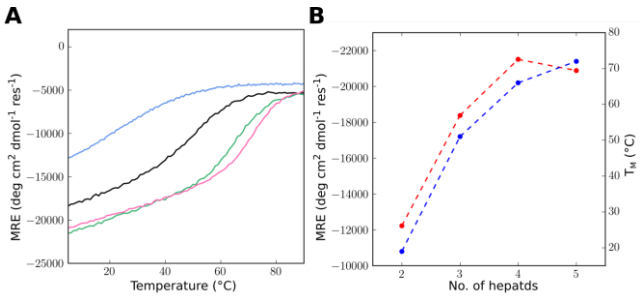

Figure 3. Folding and stability of oPPα variants of different lengths. (A) Thermal unfolding curves for oPPα-2 (blue), oPPα (black), oPPα-4 (green), and oPPα-5 (pink). (B) Plot of heptad length vs T_M (blue) and MRE_{222} at 5 °C (red). Conditions: 100 μM peptide, PBS, pH 7.4.

There is a periodicity mismatch between the 3- and 7- residue sequence repeats of polyproline-II and α helices: the former span ≈ 9.3 Å and the latter ≈ 10.5 Å. For oPPα-5 this could result in a ≈6 Å discrepancy over the lengths of the helices in the interface. The bacterial adhesin AgI/II from *S. mutans* overcomes this with Pro insertions that break the PXX repeat.[16] Therefore, we introduced an extra Pro to the middle of the polyproline-II repeat of oPPα-5. This peptide, oPPα-5-skip, was monomeric, folded and stable (Figure S2S,T) but had a slightly lower T_M than the parent. This suggests that the helix-helix interface of the oPPα fold is plastic and accommodates minor mismatches in periodicities, perhaps not possible for longer, fibrous assemblies.

In summary, a miniprotein fold has been optimized by rational protein redesign to give oPPα, a completely *de novo* framework with significantly enhanced thermal stability relative to the parent design. We propose that complementary long-range electrostatic interactions and increased shorter-range noncovalent interactions are responsible for the enhanced stability. The specific sequence-to-structure/stability relationships that we have explored should help guide further designs of PPα-like miniproteins. oPPα should be a useful addition to the toolkit of synthetic peptide building blocks for constructing more-complex systems through modular assembly.[31, 32]

ASSOCIATED CONTENT

Supporting Information

The Supporting Information is available free of charge on the ACS Publications website.

Experimental details and characterization data.

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Notes

The authors declare no competing financial interest.

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